

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/588,542
Source: IFWP
Date Processed by STIC: 8/14/06

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IFWP

RAW SEQUENCE LISTING

DATE: 08/14/2006

PATENT APPLICATION: US/10/588,542

TIME: 13:50:47

Input Set : A:\2006-1298A HIDA Sequence Listing.txt

Output Set: N:\CRF4\08142006\J588542.raw

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3 <110> APPLICANT: EISAI CO., LTD.
5 <120> TITLE OF INVENTION: Screening method
7 <130> FILE REFERENCE: E1-A0410Y1P
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/588,542
C--> 9 <141> CURRENT FILING DATE: 2006-08-07
9 <150> PRIOR APPLICATION NUMBER: JP 2004-31591
10 <151> PRIOR FILING DATE: 2004-02-09
12 <150> PRIOR APPLICATION NUMBER: JP 2004-368509
13 <151> PRIOR FILING DATE: 2004-12-20
16 <160> NUMBER OF SEQ ID NOS: 14
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 429
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(429)
28 <223> OTHER INFORMATION:
W--> 30 <400> 1
31 atg gcc agg tac atg ctg ctg ctg ctc ctg gcg gta tgg gtg ctg acc      48
32 Met Ala Arg Tyr Met Leu Leu Leu Leu Leu Ala Val Trp Val Leu Thr
33 1 5 10 15
35 ggg gag ctg tgg ccg gga gct gag gcc cgg gca gcg cct tac ggg gtc      96
36 Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val
37 20 25 30
39 agg ctt tgc ggc cga gaa ttc atc cga gca gtc atc ttc acc tgc ggg      144
40 Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly
41 35 40 45
43 ggc tcc cgg tgg aga cga tca gac atc ctg gcc cac gag gct atg gga      192
44 Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly
45 50 55 60
47 gat acc ttc ccg gat gca gat gct gat gaa gac agt ctg gca ggc gag      240
48 Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu
49 65 70 75 80
51 ctg gat gag gcc atg ggg tcc agc gag tgg ctg gcc ctg acc aag tca      288
52 Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser
53 85 90 95
55 ccc cag gcc ttt tac agg ggg cga ccc agc tgg caa gga acc cct ggg      336
56 Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly
57 100 105 110
59 gtt ctt cgg ggc agc cga gat gtc ctg gct ggc ctt tcc agc agc tgc      384
60 Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys

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61          115          120          125
63 tgc aag tgg ggg tgt agc aaa agt gaa atc agt agc ctt tgc tag      429
64 Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys
65          130          135          140
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 142
70 <212> TYPE: PRT
71 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2
75 Met Ala Arg Tyr Met Leu Leu Leu Leu Leu Ala Val Trp Val Leu Thr
76 1          5          10          15
79 Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val
80          20          25          30
83 Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly
84          35          40          45
87 Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly
88          50          55          60
91 Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu
92 65          70          75          80
95 Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser
96          85          90          95
99 Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly
100          100          105          110
103 Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys
104          115          120          125
107 Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys
108          130          135          140
111 <210> SEQ ID NO: 3
112 <211> LENGTH: 1857
113 <212> TYPE: DNA
114 <213> ORGANISM: Homo sapiens
116 <220> FEATURE:
117 <221> NAME/KEY: CDS
118 <222> LOCATION: (361)..(1770)
119 <223> OTHER INFORMATION:
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122 gatttgggga gttatgcgcc agtgccccag tgaccgcggg acacggagag gggaagtctg      60
124 cgttgtacat aaggacctag ggactccgag cttggcctga gaacccttgg acgccgagtg      120
126 cttgccttac gggctgcaact cctcaactct gctccaaagc agccgctgag ctcaactcct      180
128 gcgtccaggg cgttcgtcgc gcgccaggac gcgcttagta cccagttcct gggctctctc      240
130 ttcagtagct gctttgaaag ctcccacgca cgtcccgcag gctagcctgg caacaaaact      300
132 ggggtaaacc gtgttatctt aggtcttgtc cccagaaca tgacctagag gtacctgcgc      360
134 atg cag atg gcc gat gca gcc acg ata gcc acc atg aat aag gca gca      408
135 Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala
136 1          5          10          15
138 ggc ggg gac aag cta gca gaa ctc ttc agt ctg gtc ccg gac ctt ctg      456
139 Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu
140          20          25          30
142 gag gcg gcc aac acg agt ggt aac gcg tcg ctg cag ctt ccg gac ttg      504

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143	Glu	Ala	Ala	Asn	Thr	Ser	Gly	Asn	Ala	Ser	Leu	Gln	Leu	Pro	Asp	Leu	
144			35					40					45				
146	tgg	tgg	gag	ctg	ggg	ctg	gag	ttg	ccg	gac	ggc	gcg	ccg	cca	gga	cat	552
147	Trp	Trp	Glu	Leu	Gly	Leu	Glu	Leu	Pro	Asp	Gly	Ala	Pro	Pro	Gly	His	
148		50					55					60					
150	ccc	ccg	ggc	agc	ggc	ggg	gca	gag	agc	gcg	gac	aca	gag	gcc	cgg	gtg	600
151	Pro	Pro	Gly	Ser	Gly	Gly	Ala	Glu	Ser	Ala	Asp	Thr	Glu	Ala	Arg	Val	
152	65					70					75				80		
154	cgg	att	ctc	atc	agc	gtg	gtg	tac	tgg	gtg	gtg	tgc	gcc	ctg	ggg	ttg	648
155	Arg	Ile	Leu	Ile	Ser	Val	Val	Tyr	Trp	Val	Val	Cys	Ala	Leu	Gly	Leu	
156					85				90					95			
158	gcg	ggc	aac	ctg	ctg	gtt	ctc	tac	ctg	atg	aag	agc	atg	cag	ggc	tgg	696
159	Ala	Gly	Asn	Leu	Leu	Val	Leu	Tyr	Leu	Met	Lys	Ser	Met	Gln	Gly	Trp	
160			100						105					110			
162	cgc	aag	tcc	tct	atc	aac	ctc	ttc	gtc	acc	aac	ctg	gcg	ctg	acg	gac	744
163	Arg	Lys	Ser	Ser	Ile	Asn	Leu	Phe	Val	Thr	Asn	Leu	Ala	Leu	Thr	Asp	
164			115						120					125			
166	ttt	cag	ttt	gtg	ctc	acc	ctg	ccc	ttc	tgg	gcg	gtg	gag	aac	gct	ctt	792
167	Phe	Gln	Phe	Val	Leu	Thr	Leu	Pro	Phe	Trp	Ala	Val	Glu	Asn	Ala	Leu	
168		130					135					140					
170	gac	ttc	aaa	tgg	ccc	ttc	ggc	aag	gcc	atg	tgt	aag	atc	gtg	tcc	atg	840
171	Asp	Phe	Lys	Trp	Pro	Phe	Gly	Lys	Ala	Met	Cys	Lys	Ile	Val	Ser	Met	
172	145					150				155				160			
174	gtg	acg	tcc	atg	aac	atg	tac	gcc	agc	gtg	ttc	ttc	ctc	act	gcc	atg	888
175	Val	Thr	Ser	Met	Asn	Met	Tyr	Ala	Ser	Val	Phe	Phe	Leu	Thr	Ala	Met	
176					165					170				175			
178	agt	gtg	acg	cgc	tac	cat	tcg	gtg	gcc	tcg	gct	ctg	aag	agc	cac	cgg	936
179	Ser	Val	Thr	Arg	Tyr	His	Ser	Val	Ala	Ser	Ala	Leu	Lys	Ser	His	Arg	
180			180						185					190			
182	acc	cga	gga	cac	ggc	cgg	ggc	gac	tgc	tgc	ggc	cgg	agc	ctg	ggg	gac	984
183	Thr	Arg	Gly	His	Gly	Arg	Gly	Asp	Cys	Cys	Gly	Arg	Ser	Leu	Gly	Asp	
184			195					200					205				
186	agc	tgc	tgc	ttc	tcg	gcc	aag	gcg	ctg	tgt	gtg	tgg	atc	tgg	gct	ttg	1032
187	Ser	Cys	Cys	Phe	Ser	Ala	Lys	Ala	Leu	Cys	Val	Trp	Ile	Trp	Ala	Leu	
188		210					215					220					
190	gcc	gcg	ctg	gcc	tcg	ctg	ccc	agt	gcc	att	ttc	tcc	acc	acg	gtc	aag	1080
191	Ala	Ala	Leu	Ala	Ser	Leu	Pro	Ser	Ala	Ile	Phe	Ser	Thr	Thr	Val	Lys	
192	225					230					235			240			
194	gtg	atg	ggc	gag	gag	ctg	tgc	ctg	gtg	cgt	ttc	ccg	gac	aag	ttg	ctg	1128
195	Val	Met	Gly	Glu	Glu	Leu	Cys	Leu	Val	Arg	Phe	Pro	Asp	Lys	Leu	Leu	
196				245					250					255			
198	ggc	cgc	gac	agg	cag	ttc	tgg	ctg	ggc	ctc	tac	cac	tcg	cag	aag	gtg	1176
199	Gly	Arg	Asp	Arg	Gln	Phe	Trp	Leu	Gly	Leu	Tyr	His	Ser	Gln	Lys	Val	
200			260						265					270			
202	ctg	ttg	ggc	ttc	gtg	ctg	ccg	ctg	ggc	atc	att	atc	ttg	tgc	tac	ctg	1224
203	Leu	Leu	Gly	Phe	Val	Leu	Pro	Leu	Gly	Ile	Ile	Ile	Leu	Cys	Tyr	Leu	
204			275					280						285			
206	ctg	ctg	gtg	cgc	ttc	atc	gcc	gac	cgc	cgc	gcg	gcg	ggg	acc	aaa	gga	1272
207	Leu	Leu	Val	Arg	Phe	Ile	Ala	Asp	Arg	Arg	Ala	Ala	Gly	Thr	Lys	Gly	

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208      290      295      300
210 ggg gcc gcg gta gcc gga gga cgc ccg acc gga gcc agc gcc cgg aga      1320
211 Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg
212 305      310      315      320
214 ctg tcg aag gtc acc aaa tca gtg acc atc gtt gtc ctg tcc ttc ttc      1368
215 Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe
216      325      330      335
218 ctg tgt tgg ctg ccc aac cag gcg ctc acc acc tgg agc atc ctc atc      1416
219 Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile
220      340      345      350
222 aag ttc aac gcg gtg ccc ttc agc cag gag tat ttc ctg tgc cag gta      1464
223 Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val
224      355      360      365
226 tac gcg ttc cct gtg agc gtg tgc cta gcg cac tcc aac agc tgc ctc      1512
227 Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
228      370      375      380
230 aac ccc gtc ctc tac tgc ctc gtg cgc cgc gag ttc cgc aag gcg ctc      1560
231 Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu
232 385      390      395      400
234 aag agc ctg ctg tgg cgc atc gcg tct cct tcg atc acc agc atg cgc      1608
235 Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg
236      405      410      415
238 ccc ttc acc gcc act acc aag ccg gag cac gag gat cag ggg ctg cag      1656
239 Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln
240      420      425      430
242 gcc ccg gcg ccg ccc cac gcg gcc gcg gag ccg gac ctg ctc tac tac      1704
243 Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
244      435      440      445
246 cca cct ggc gtc gtg gtc tac agc ggg ggg cgc tac gac ctg ctg ccc      1752
247 Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
248      450      455      460
250 agc agc tct gcc tac tga cgcaggcctc aggcccaggg cgcgcgctcg      1800
251 Ser Ser Ser Ala Tyr
252 465
254 gggcaagggtg gccttccccg ggcggtaaag aggtgaaagg atgaaggagg gctgggg      1857
257 <210> SEQ ID NO: 4
258 <211> LENGTH: 469
259 <212> TYPE: PRT
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 4
264 Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala
265 1      5      10      15
268 Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu
269      20      25      30
272 Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu
273      35      40      45
276 Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His
277      50      55      60
280 Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val

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281 65          70          75          80
284 Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu
285          85          90          95
288 Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp
289          100          105          110
292 Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp
293          115          120          125
296 Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu
297          130          135          140
300 Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met
301 145          150          155          160
304 Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met
305          165          170          175
308 Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg
309          180          185          190
312 Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp
313          195          200          205
316 Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu
317          210          215          220
320 Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys
321 225          230          235          240
324 Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu
325          245          250          255
328 Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val
329          260          265          270
332 Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu
333          275          280          285
336 Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly
337          290          295          300
340 Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg
341 305          310          315          320
344 Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe
345          325          330          335
348 Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile
349          340          345          350
352 Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val
353          355          360          365
356 Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu
357          370          375          380
360 Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu
361 385          390          395          400
364 Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg
365          405          410          415
368 Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln
369          420          425          430
372 Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr
373          435          440          445
376 Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro
377          450          455          460

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VERIFICATION SUMMARY

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Input Set : A:\2006-1298A HIDA Sequence Listing.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28

L:121 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:119